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*Virulence- Addendum*

## Haptoglobin-Hemoglobin Receptor Independent Killing of African Trypanosomes by Human Serum and Trypanosome Lytic Factors

Whitney Bullard<sup>1</sup>, Rudo Kieft<sup>1</sup>, Paul Capewell<sup>2</sup>, Nicola J. Veitch<sup>2</sup>, Annette Macleod<sup>2\*</sup> and Stephen L. Hajduk<sup>1\*</sup>

<sup>1</sup>Department of Biochemistry and Molecular Biology, University of Georgia, Athens GA USA; <sup>2</sup>Faculty of Veterinary Medicine, Wellcome Centre for Molecular Parasitology, Glasgow G61 1QH, UK

\*Correspondence to: Either Annette Macleod or Stephen Hajduk

Email: [gywa08@udcf.gla.ac.uk](mailto:gywa08@udcf.gla.ac.uk) or [shajduk@bmb.uga.edu](mailto:shajduk@bmb.uga.edu)

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## ABSTRACT

The haptoglobin-hemoglobin receptor (HpHbR) of African trypanosomes plays a critical role in human innate immunity against these parasites. Localized to the flagellar pocket of the veterinary pathogen *Trypanosoma brucei brucei* this receptor binds Trypanosome Lytic Factor-1 (TLF-1), a subclass of human high-density lipoprotein (HDL) facilitating endocytosis, lysosomal trafficking and subsequent killing. Recently, we found that group 1 *Trypanosoma brucei gambiense*, does not express a functional HpHbR. We now show that loss of the *TbbHpHbR* reduces the susceptibility of *T. b. brucei* to human serum and TLF-1 by 100 and 10,000 fold respectively. The relatively high concentrations of human serum and TLF-1 needed to kill trypanosomes lacking the HpHbR indicates that high affinity *TbbHpHbR* binding enhances the cytotoxicity, however in the absence of *TbbHpHbR* other receptors or fluid phase endocytosis are sufficient to provide some level of susceptibility. Human serum contains a second innate immune factor, TLF-2, that has been suggested to kill trypanosomes independently of the *TbbHpHbR*. We found that *T. b. brucei* killing by TLF-2 was reduced in *TbbHpHbR* deficient cells but to a lesser extent than TLF-1. This suggests that both TLF-1 and TLF-2 can be taken up via the *TbbHpHbR* but that alternative pathways exist for the uptake of these toxins. Together the findings reported here extend our previously published studies (Kieft *et al.*, 2010) and suggest that group 1 *T. b. gambiense* has evolved multiple mechanisms to avoid killing by trypanolytic human serum factors.

## INTRODUCTION

African trypanosomes are eukaryotic pathogens that cause important human and animal diseases. These parasites have evolved a variety of mechanisms to escape innate and acquired immunity including the use of the variant surface glycoprotein (VSG) coat to cover the plasma membrane of the parasite providing a barrier against attack by complement<sup>1</sup>. The VSG coat also serves as the molecular decoy during antigenic variation presenting an ever-changing target to the adaptive immune system of the mammal, thus allowing the parasites to evade antibody mediated killing<sup>2</sup>. The subspecies of trypanosomes that infect humans face the additional challenge of encountering a unique innate defense mechanism mediated by two related serum proteins complexes. In the circulation of humans, TLF-1 is a minor subclass of HDL containing apolipoprotein A-1 (apoA-1), the defining protein of all HDLs, and two primate specific proteins, apolipoprotein L-1 (apoL-1) and haptoglobin-related protein (Hpr)<sup>3,4,5,6,7</sup>. In addition to these apolipoproteins, Hpr binds free hemoglobin (Hb) in the circulation, which is likely released from erythrocytes during early infection<sup>8</sup>. The heterodimeric Hpr/Hb complex is proposed to be bifunctional, serving both as the ligand for the *T. b. brucei* HpHbR<sup>9,10</sup> and directly contributing to high specific activity killing by catalyzing the peroxidation of lysosomal membrane lipids<sup>6,7,11</sup>. The other primate specific apolipoprotein in TLF-1, apoL-1, is also directly involved in *T. b. brucei* killing<sup>5,12,13</sup>. An ion channel forming protein, apoL-1 undergoes conformation changes at lysosomal pH and can integrate into membranes<sup>5,12,14</sup>. The combined action of Hpr/Hb and apoL-1 results in the osmotic lysis of the parasite<sup>15,16</sup>. The other



trypanolytic serum complex is called TLF-2 and, while largely devoid of lipids it contains Hpr and apoA-1<sup>17</sup> and apoL-1 (this paper) suggesting that these complexes share a common origin and perhaps have a similar mechanism of trypanosome killing<sup>18</sup>.

The two subspecies of human sleeping sickness trypanosomes have evolved distinct mechanisms to survive in the human host. *Trypanosoma brucei rhodesiense* produces the serum resistance associated (SRA) protein that binds and inhibits TLF-1<sup>19,20,21</sup>. SRA, an intracellular protein largely found in endosomes, co-localizes with TLF-1 in early endosomes and trafficks to the lysosome<sup>22</sup>. Thus, *T. b. rhodesiense* survives in humans largely because it is able to produce an antidote to TLF-1. While untested, it is likely that TLF-2 is inhibited by SRA by the same mechanism since both serum complexes contain apoL-1. In contrast, we recently showed that group 1 *T. b. gambiense* does not bind or take up TLF-1 suggesting that these cells have evolved a different mechanism to avoid the cytotoxicity of TLF-1<sup>23</sup>. The underlying basis for reduced TLF-1 uptake is two fold. First, *TbgHpHpR* is expressed at very low levels by group 1 *T. b. gambiense* and second, *TbgHpHbR* contains a number of point mutations within the coding sequence, that render the receptor non-functional<sup>23</sup>. The combination of mutations to the *TbgHpHbR* and reduced expression abolished TLF-1 binding and uptake resulting in resistance to TLF-1. Thus, in contrast to *T. b. rhodesiense*, it appears the mechanism of group 1 *T. b. gambiense* resistance to TLF-1 involves reduced uptake and avoidance of the toxin. To date no evidence for an inhibitory protein with SRA-like characteristics has been described in *T. b. gambiense*. In this short addendum to the Kieft *et al.* (2010) paper

we now show that while the *TbbHpHbR* enhances susceptibility to human serum, TLF-2 and TLF-1 other receptors or fluid phase endocytosis also contribute to trypanosome killing. Further, our results suggest that the resistance of group 1 *T. b. gambiense* to human serum and TLF involves other mechanisms beyond the simple loss of a single receptor.

## **MATERIAL & METHODS**

*TLF-1 and TLF-2 Purification.* Total serum was obtained from a healthy human donor. As previously described, two sequential flotations on sodium bromide gradients ( $\rho=1.063$  and  $1.26$  g/ml) resulted in an HDL-rich fraction (TLF-1; top third of the gradient) and a lipoprotein deficient fraction (TLF-2; bottom third of the gradient)<sup>4</sup>. The TLF-1 fraction was passed over an anti-IgM column (Sigma, A9935). The unbound material was then passed over an anti-Hpr column, washed with PBSE (137 mM NaCl, 2.7 mM KCl, 10 mM Na<sub>2</sub>HPO<sub>4</sub>, 10 mM KH<sub>2</sub>PO<sub>4</sub>, 3 mM EDTA) and bound protein was eluted in 100 mM glycine (pH 2.5) and neutralized with 1 M Tris (pH 7.5). The TLF-2 fraction was passed over an anti-Hpr column and washed with PBSE. Bound protein was eluted in 100 mM glycine (pH 2.5), neutralized with 1 M Tris (pH 7.5) and immediately added to an anti-IgM column and washed with PBSE. Bound protein was eluted in 100 mM glycine (pH 2.5), neutralized with 1 M Tris (pH 7.5). All protein samples were aliquoted and stored at -80°C.

*Size Exclusion Chromatography and Western Blot Analysis.* Size exclusion chromatography was performed on a 1 X PBSE equilibrated Superose 6 10/300 GL column (GE Healthcare). Individual protein standards were used to estimate the molecular weights of TLF-1 and TLF-2. Samples of TLF-1 and TLF-2 from immuno-affinity purification (70 µg) were run on the Superose 6 column at a flow rate of 0.5 ml/min. Fractions were collected (0.5 ml), proteins concentrated six fold with microspin S-300HR columns (GE, 27513001) and the distribution of Hpr, apoL-1 and IgM determined by SDS-PAGE, silver staining and western blot analysis. Characterization of antibodies against Hpr and apoL-1 has previously been described<sup>7</sup>. Anti-IgM was purchased from Sigma and used according to the manufacturers recommendation (Sigma, I0759).

## RESULTS

*TLF-1 resistant T. b. brucei.* During the course of our studies on the mechanism of TLF-1 resistance in group 1 *T. b. gambiense* we developed a laboratory model for TLF-1 resistance using well-characterized clonal cell lines of *T. b. brucei* that had been selected for resistance to human HDLs<sup>23,24</sup>. We isolated TLF-1 resistant (R) or susceptible (S) *T. b. brucei* lines expressing either the VSG800 or VSG060<sup>23</sup>. The *T. b. brucei* 427-800<sup>R</sup> and *T. b. brucei* 427-060<sup>R</sup> lines showed reduced uptake of TLF-1 relative to the TLF-1 susceptible parental *T. b. brucei* 427-221<sup>S</sup> cells and TLF-1 susceptible cells expressing either VSG800 or VSG060. In addition, we showed that the expression of *TbbHpHbR* mRNA was reduced approximately 20-fold in resistant cells<sup>23</sup>. These findings led us to examine group 1 *T. b. gambiense* where we found

that not only was expression of the *TbgHbR* mRNA reduced but that mutations to the gene abolished function <sup>23</sup>.

*Purification and characterization of TLF-1 and TLF-2.* In order to determine whether loss of *TbbHbR* was sufficient to provide complete protection from human serum, TLF-1 and TLF-2 activity we developed a purification protocol exploiting physical and compositional differences in these human serum innate immune complexes (Figure 1). Freshly collected human plasma was initially separated by density gradient ultracentrifugation to produce HDL-enriched ( $\rho$  1.063 – 1.26 g/ml) and lipoprotein-deficient fractions ( $\rho$  <1.063 g/ml) that were used as the starting materials for TLF-1 and TLF-2 purification respectively. During the purification of TLF-1 small amounts of contaminating TLF-2 were removed from the HDL-containing fraction by absorption with anti-IgM. TLF-1 was subsequently bound to anti-Hpr resin, washed extensively at neutral pH to remove human HDLs lacking Hpr and eluted at low pH. TLF-2 was purified from the lipoprotein-deficient serum by sequential affinity chromatography with anti-Hpr followed by binding and elution from an anti-IgM column. The purity of TLF-1 and TLF-2 was evaluated by size exclusion chromatography on Superose 6 and western blot analysis with anti-Hpr, apoL-1 and IgM (Figure 1A and B). Based on size exclusion chromatography TLF-1 and TLF-2 have estimated relative sizes of 576KDa and 1.6MDa respectively<sup>17</sup>. Superose 6 chromatography of purified TLF-1 and TLF-2 revealed somewhat dispersed distributions consistent with particle heterogeneity but there was minimal overlap of the TLF-1 and TLF-2 absorbance peaks at 280nm (Figure 1A). Western blot analysis revealed no contaminating TLF-2 in our purified TLF-1

preparations based on the lack of anti-IgM reactive material on western blots (Figure 1B; data not shown). TLF-2 preparations were highly enriched in particles containing Hpr, apoL-1 and IgM, however, these preparations also contained small amounts of IgM deficient complexes with an elution time (~28 min) from the Superose 6 column consistent with TLF-1. Based on the distribution of the Hpr dimer and IgM across the size exclusion fractions we estimate the amount of contaminating TLF-1 in these preparations to be ~10%.

*Susceptibility of T. b. brucei to human serum, TLF-1 and TLF-2.* Our previous studies compared the short-term killing of trypanosomes to TLF-1<sup>23</sup>. Here we have reexamined the susceptibility of these *T. b. brucei* lines using a long-term growth assay (Figure 2). Consistent with previous studies, the parental *T. b. brucei* 427-221<sup>S</sup>, *T. b. brucei* 427-800<sup>S</sup>, and *T. b. brucei* 427-060<sup>S</sup> were highly susceptible to TLF-1 with a calculated LG<sub>50</sub> of 0.8-6 ng/ml. *T. b. brucei* 427-800<sup>R</sup> and *T. b. brucei* 427-060<sup>R</sup> were >10,000 fold more resistant to TLF-1 than wild type *T. b. brucei* suggesting the *TbbHpHbR* is important in TLF-1 susceptibility. However, concentrations of >10 µg/ml overcame the *TbbHpHbR* deficiency leading to reduced survival (Figure 2A). Since the concentration of TLF-1 needed to kill *T. b. brucei* 427-800<sup>R</sup> and *T. b. brucei* 427-060<sup>R</sup> is similar to that found in human serum it is likely that, *TbbHpHbR* independent mechanisms of TLF-1 uptake play a significant role in trypanosome killing.

Based on our studies with both the group 1 *T. b. gambiense* and the TLF-1 resistant *T. b. brucei* lines we predicted that loss of a functional *TbgHpHbR* played a critical

role in human infection by African trypanosomes<sup>23</sup>. The dramatic reduction in susceptibility to TLF-1 in the *TbbHpHbR* deficient cell lines supports this prediction (Figure 2A). However, the possibility remained that human serum contained additional innate immune factors, such as TLF-2, that might not require the *TbbHpHbR*. To test this possibility, we treated TLF-1 resistant and susceptible *T. b. brucei* lines with human serum (Figure 2B). We found that *T. b. brucei* 427-800<sup>R</sup> and *T. b. brucei* 427-060<sup>R</sup> were approximately 100 fold more resistant to human serum killing than either *T. b. brucei* 427-800<sup>S</sup> or *T. b. brucei* 427-060<sup>S</sup> (Figure 2B). Based on these results, we conclude that loss of *TbbHpHbR* expression contributes to the overall resistance of these cells to human serum, however the level of resistance is much less than the high level of resistance seen for TLF-1 (10,000 fold). A possible interpretation of these findings is that other human serum components, such as TLF-2, are less dependent on *TbbHpHbR* binding than TLF-1.

It has been proposed that TLF-2 can bind to *T. b. brucei* in the absence of the *TbbHpHbR*<sup>18</sup>. We tested whether highly purified TLF-2 was able to kill *T. b. brucei* 427-800<sup>R</sup> and *T. b. brucei* 427-060<sup>R</sup> (Figure 2C). Similar to our findings with complete human serum, these *TbbHpHbR* deficient cells were more resistant to TLF-2 relative to the wildtype, *TbbHpHbR* expressing, cell lines. Thus, reduced expression of *TbbHpHbR* expression caused a reduced susceptibility of TLF-2 killing suggesting that TLF-2 can bind to the *TbbHpHbR*. However, the toxic concentration of TLF-2 is >10 fold less than TLF-1 indicating that *TbbHpHbR* independent mechanisms may play a greater role in TLF-2 binding, uptake and killing.

## DISCUSSION

In the studies presented here human serum, TLF-1 and TLF-2 susceptibility was examined in isogenic lines of *T. b. brucei* differing in *TbbHpHbR* expression. Cells deficient in *TbbHpHbR* expression were 10,000 fold more resistant to TLF-1 relative to wild type, susceptible cells. However, at concentrations of TLF-1 typically found in serum ( $>10\mu\text{g/ml}$ ), both resistant and susceptible cell lines were killed. Human serum killing was also reduced approximately 100 fold in cell lines expressing reduced levels of *TbbHpHbR*. However, significant killing was still observed at human serum concentrations above  $100\mu\text{g/ml}$ . Since the only difference in the susceptible and resistance cell lines is the levels of expression of *TbbHpHbR* it seems likely that human serum contains a second trypanolytic activity that interacts with *T. b. brucei* independently of the *TbbHpHbR*. Based on this interpretation of the human serum killing results we decided to investigate whether TLF-2 killing of *T. b. brucei* was independent on the level of expression of *TbbHpHbR*. We found that TLF-2 killing was reduced 500-1000 fold in cell lines with reduced levels of *TbbHpHbR* suggesting that TLF-2 also binds *TbbHpHbR*. These results are in apparent contrast to previous studies on TLF-2 showing that TLF-2 killing was not inhibited by the addition of haptoglobin, an inhibitor of HpHb binding to the *TbbHpHbR*<sup>17</sup>. These results have been used subsequently to argue that TLF-2 does not bind the *TbbHpHbR*<sup>10</sup>. It is possible that our results are influenced by the small amount of contaminating TLF-1 in our TLF-2 preparations. Clearly, a detailed characterization of the TLF-2 binding, uptake and cellular location is needed.

Our results are consistent with previous findings indicating the importance of the *TbbHpHbR* in TLF-1 killing but also suggest that other mechanisms of TLF-1 binding and uptake may contribute to trypanosome killing. The most likely pathways for *TbbHpHbR* independent uptake of TLF-1 is either by fluid phase endocytosis or the trypanosome lipoprotein scavenger receptor<sup>25,18</sup>. The findings presented here further support the findings of others that TLF-2 killing is less dependent on the *TbbHpHbR* than is TLF-1<sup>17,10</sup>. Finally, we propose that group 1 *T. b. gambiense* have evolved multiple mechanisms, including but not limited to the loss of a functional *HpHbR*, to avoid the cytotoxicity of the trypanosome lytic factors. We are currently exploring these mechanisms.

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## FIGURE LEGENDS

**Figure 1.** Characterization of purified TLF-1 and TLF-2. **(A)** Superose 6 size exclusion chromatography of TLF-1 and TLF-2. Absorbance profiles (280 nM) of TLF-1 and TLF-2, superimposed on individually ran marker proteins (1 = thyroglobulin (660kDa), 2 = apoferritin (480kDa), 3 = conalbumin (67kDa), 4 = ovalbumin (45kDa). **(B)** Analysis of individual Superose 6 column fractions of TLF-1 and TLF-2 separated on non-denaturing 12% SDS-PAGE and silver stained (top panel). Hpr, apoL1 and IgM were detected by western blot. (NA = indicates samples that were not analyzed)

**Figure 2.** *In vitro* activity of human serum, TLF-1 and TLF-2. TLF-1 resistant (R) and susceptible (S) clonal cell lines of bloodstream form *T. b. brucei* Lister 427 expressing VSG221, 800 and 060 were prepared as previously described<sup>24,25</sup>. The percentage surviving cells was determined, using phase contrast microscopy, 14 hours following the addition of TLF-1, TLF-2 or complete human serum to exponentially growing cultures at 37°C. **(A)** TLF-1 susceptibility of *T. b. brucei* 427-221<sup>S</sup> (black), *T. b. brucei* 427-800<sup>S</sup> (blue), *T. b. brucei* 427-800<sup>R</sup> (red), *T. b. brucei* 427-060<sup>S</sup> (yellow) and 427-060<sup>R</sup> (green). **(B)** Normal human serum (NHS) susceptibility of *T. b. brucei* 427-221<sup>S</sup> (black), *T. b. brucei* 427-800<sup>S</sup> (blue), *T. b. brucei*

427-800<sup>R</sup> (red), *T. b. brucei* 427-060<sup>S</sup> (yellow) and 427-060<sup>R</sup> (green). **(C)** TLF-2 susceptibility of *T. b. brucei* 427-221<sup>S</sup> (black), *T. b. brucei* 427-800<sup>S</sup> (blue), *T. b. brucei* 427-800<sup>R</sup> (red), *T. b. brucei* 427-060<sup>S</sup> (yellow) and 427-060<sup>R</sup> (green).

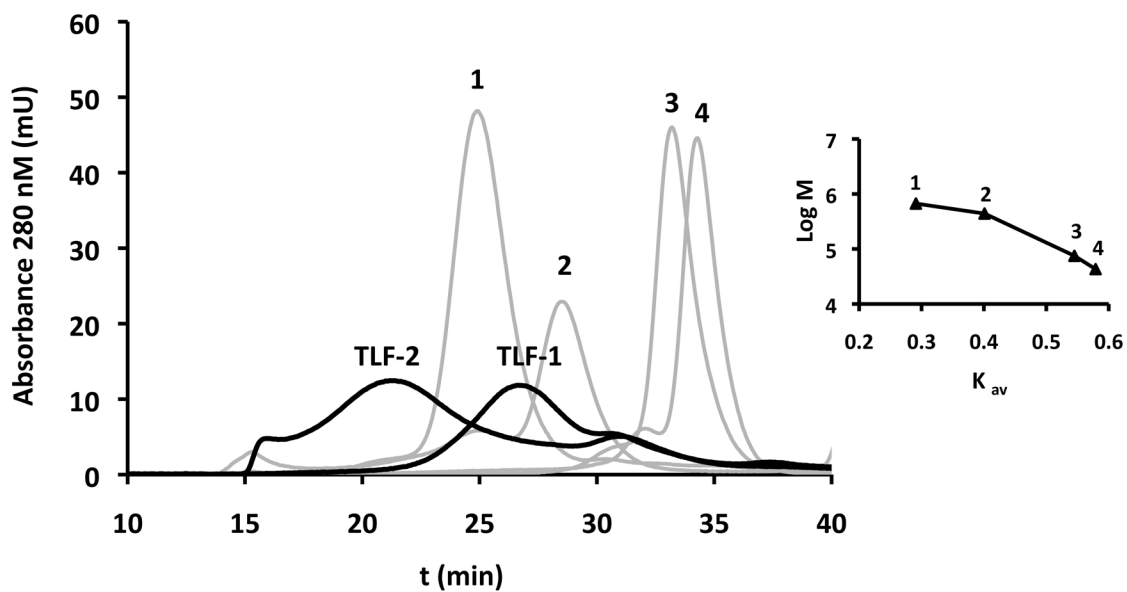
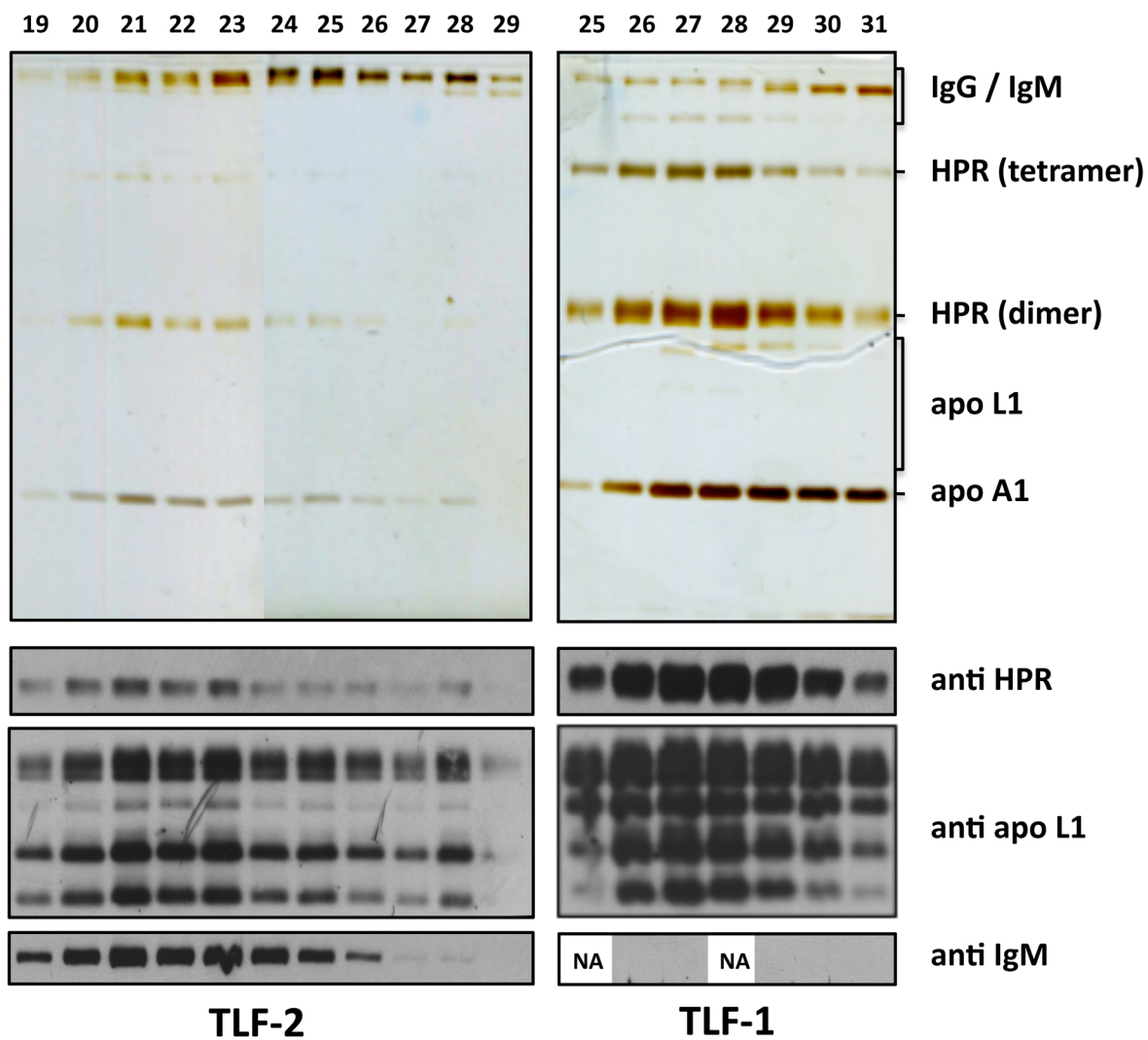
**A****B**

Figure 1

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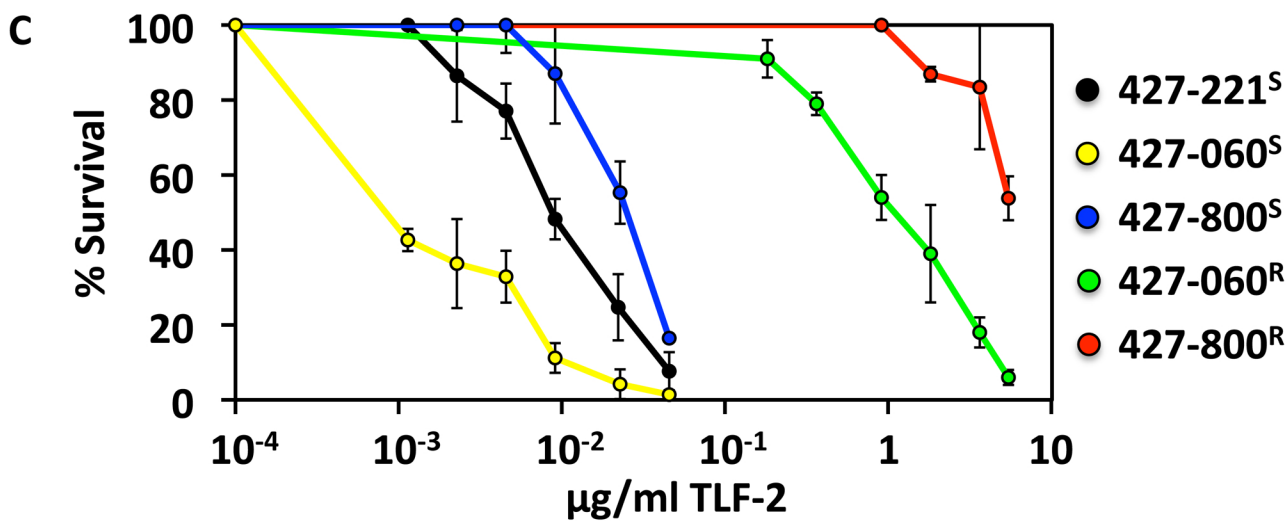
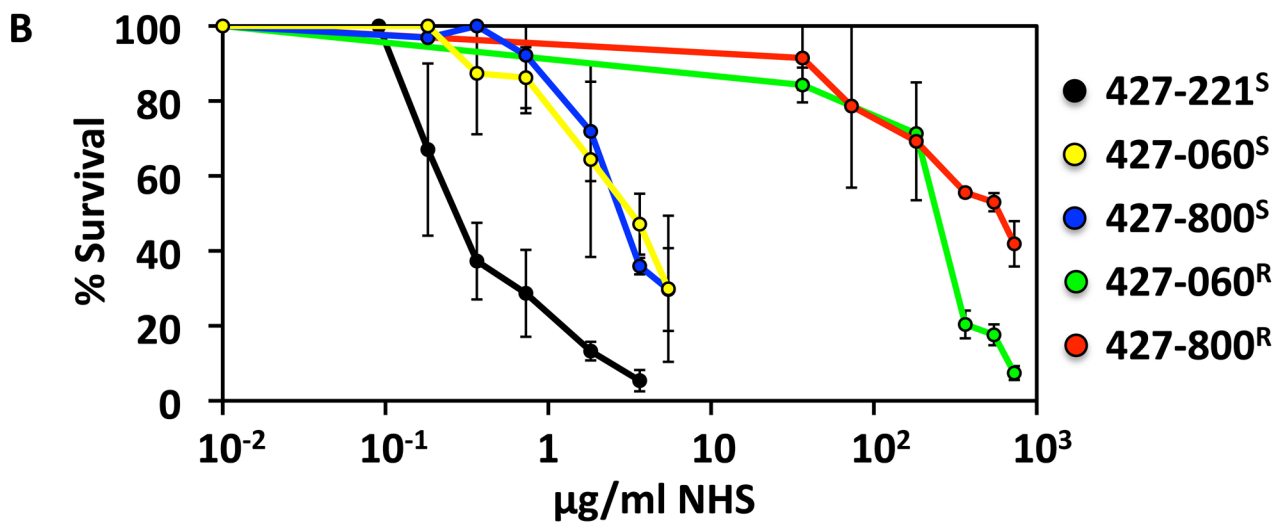
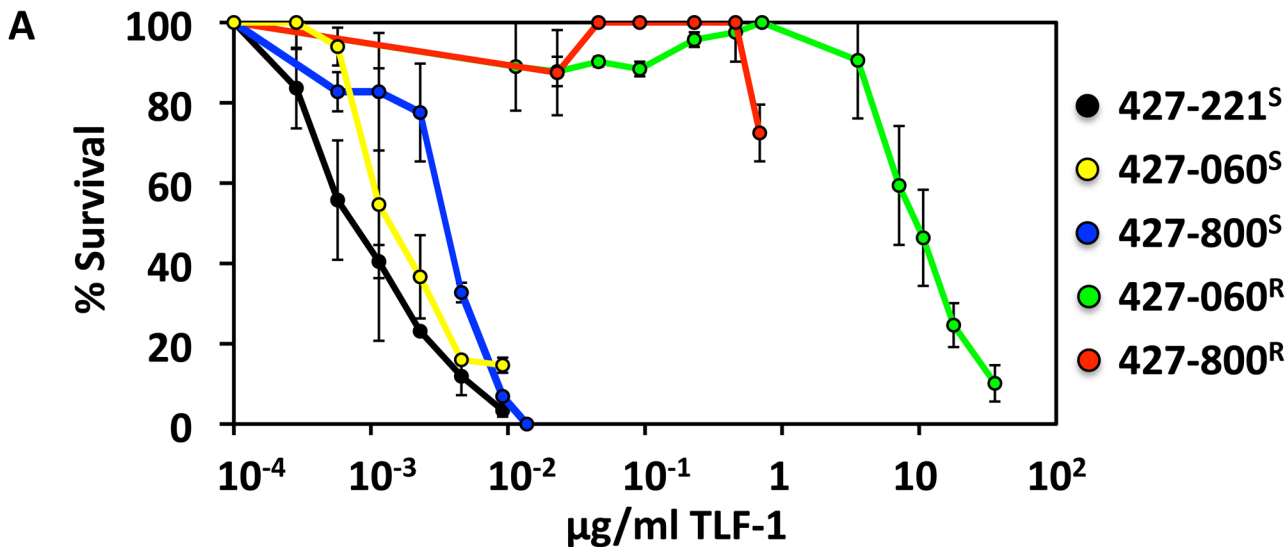


Figure 2